

Application No. 09/919,854
Reply to Office Action of August 26, 2003

IN THE CLAIMS

Claims 1-35 (Canceled):

Claim 36 (Previously Presented): An isolated polynucleotide
which is at least 90% identical to SEQ ID NO: 1, or to a fragment of SEQ ID NO: 1,
and
which encodes a polypeptide having the enzymatic activity of adenosyl
homocysteinase.

Claim 37 (Previously Presented): The isolated polynucleotide of Claim 36, which is
at least 95% identical to SEQ ID NO: 1.

Claim 38 (Previously Presented): The isolated polynucleotide of Claim 36, which
encodes the polypeptide of SEQ ID NO: 2.

Claim 39 (Previously Presented): The isolated polynucleotide of Claim 36, which
comprises nucleotides 227 to 1720 of SEQ ID NO: 1.

Claim 40 (Previously Presented): The isolated polynucleotide of Claim 36, further
comprising at least one promoter, ribosome binding site, regulatory region or expression
cassette.

Claim 41 (Previously Presented): The isolated polynucleotide of Claim 36, which is
RNA.

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Claim 42 (Previously Presented): A vector comprising the isolated polynucleotide of Claim 36.

Claim 43 (Previously Presented): A vector comprising the isolated polynucleotide of Claim 38.

Claim 44 (Previously Presented): A vector comprising the isolated polynucleotide of Claim 40.

Claim 45 (Previously Presented): A host cell comprising at least one copy of the isolated polynucleotide of Claim 36.

Claim 46 (Previously Presented): A host cell comprising multiple copies of the isolated polynucleotide of Claim 36.

Claim 47 (Previously Presented): The host cell of Claim 45, which is a coryneform bacterium.

Claim 48 (Previously Presented): The host cell of Claim 45, which is *Corynebacterium glutamicum*.

Claim 49 (Previously Presented): A process for making an amino acid comprising:
culturing the host cell of Claim 45 for a time and under conditions suitable for the
production of said amino acid, and
recovering said amino acid.

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Claim 50 (Previously Presented): The process of Claim 49, wherein said amino acid is lysine.

Claim 51 (Previously Presented): The process of Claim 49, wherein said amino acid is methionine.

Claim 52 (Currently Amended): The process of Claim 49, wherein said amino acid is lysine or methionine, and said host cell is a coryneform microorganism, which compared to an unmodified starting strain:

(A) over-expresses one or more of the following genes:

the dapA gene which codes for dihydrodipicolinate synthase,

the gap gene which codes for glyceraldehyde 3-phosphate dehydrogenase,

the tpi gene which codes for triose phosphate isomerase,

the pgk gene which codes for 3-phosphoglycerate kinase,

the zwf gene which codes for glucose 6-phosphate dehydrogenase,

the pyc gene which codes for pyruvate carboxylase,

the mqo gene which codes for malate-quinone oxidoreductase,

the lysC gene which codes for a feed-back resistant aspartate kinase,

the lysE gene which codes for lysine export,

the hom gene which codes for homoserine dehydrogenase

the ilvA gene which codes for threonine dehydratase or the ilvA(Fbr) allele which codes for a feed back resistant threonine dehydratase,

the ilvBN gene which codes for acetohydroxy-acid synthase,

the ilvD gene which codes for dihydroxy-acid dehydratase, or

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the *zwa1* gene which codes for the Zwa1 protein; and/or

(B) reduces or eliminates the expression of one or more of the following gene(s):

the *pck* gene which codes for phosphoenol pyruvate carboxykinase,

the *pgi* gene which codes for glucose 6-phosphate isomerase,

the *poxB* gene which codes for pyruvate oxidase or

the *zwa2* gene which codes for the Zwa2 protein.

Claim 53 (Previously Presented): A host cell comprising at least one copy of the isolated polynucleotide of Claim 38.

Claim 54 (Previously Presented): A host cell comprising multiple copies of the isolated polynucleotide of Claim 38.

Claim 55 (Previously Presented): The host cell of Claim 53, which is a coryneform bacterium.

Claim 56 (Previously Presented): The host cell of Claim 53, which is *Corynebacterium glutamicum*.

Claim 57 (Previously Presented): A process for making an amino acid comprising:
culturing the host cell of Claim 53 for a time and under conditions suitable for the production of said amino acid, and
recovering said amino acid.

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Claim 58 (Previously Presented): The process of Claim 57, wherein said amino acid is lysine.

Claim 59 (Previously Presented): The process of Claim 57, wherein said amino acid is methionine.

Claim 60 (Currently Amended): The process of Claim 57, wherein said amino acid is lysine or methionine, and said host cell is a coryneform microorganism, which compared to an unmodified starting strain:

(A) over-expresses one or more of the following genes:

- the dapA gene which codes for dihydrodipicolinate synthase,
- the gap gene which codes for glyceraldehyde 3-phosphate dehydrogenase,
- the tpi gene which codes for triose phosphate isomerase,
- the pgk gene which codes for 3-phosphoglycerate kinase,
- the zwf gene which codes for glucose 6-phosphate dehydrogenase,
- the pyc gene which codes for pyruvate carboxylase,
- the mqo gene which codes for malate-quinone oxidoreductase,
- the lysC gene which codes for a feed-back resistant aspartate kinase,
- the lysE gene which codes for lysine export,
- the hom gene which codes for homoserine dehydrogenase
- the ilvA gene which codes for threonine dehydratase or the ilvA(Fbr) allele which codes for a feed back resistant threonine dehydratase,
- the ilvBN gene which codes for acetohydroxy-acid synthase,
- the ilvD gene which codes for dihydroxy-acid dehydratase, or
- the zwal gene which codes for the Zwal protein; and/or

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(B) reduces or eliminates the expression of one or more of the following gene(s):

the pck gene which codes for phosphoenol pyruvate carboxykinase,

the pgi gene which codes for glucose 6-phosphate isomerase,

the poxB gene which codes for pyruvate oxidase or

the zwa2 gene which codes for the Zwa2 protein.

Claim 61 (Previously Presented): A host cell comprising at least one copy of the isolated polynucleotide of Claim 40.

Claim 62 (Previously Presented): A host cell comprising multiple copies of the isolated polynucleotide of Claim 40.

Claim 63 (Previously Presented): The host cell of Claim 61, which is a coryneform bacterium.

Claim 64 (Previously Presented): The host cell of Claim 61, which is *Corynebacterium glutamicum*.

Claim 65 (Previously Presented): A process for making an amino acid comprising:
culturing the host cell of Claim 61 for a time and under conditions suitable for the production of said amino acid, and
recovering said amino acid.

Claim 66 (Previously Presented): The process of Claim 65, wherein said amino acid is lysine.

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Claim 67 (Previously Presented): The process of Claim 65, wherein said amino acid is methionine.

Claim 68 (Currently Amended): The process of Claim 65, wherein said amino acid is lysine or methionine, and said host cell is a coryneform microorganism, which compared to an unmodified starting strain:

(A) over-expresses one or more of the following genes:

the dapA gene which codes for dihydrodipicolinate synthase,
the gap gene which codes for glyceraldehyde 3-phosphate dehydrogenase,
the tpi gene which codes for triose phosphate isomerase,
the pgk gene which codes for 3-phosphoglycerate kinase,
the zwf gene which codes for glucose 6-phosphate dehydrogenase,
the pyc gene which codes for pyruvate carboxylase,
the mqo gene which codes for malate-quinone oxidoreductase,
the lysC gene which codes for a feed-back resistant aspartate kinase,
the lysE gene which codes for lysine export,
the hom gene which codes for homoserine dehydrogenase
the ilvA gene which codes for threonine dehydratase or the ilvA(Fbr) allele which codes for a feed back resistant threonine dehydratase,
the ilvBN gene which codes for acetohydroxy-acid synthase,
the ilvD gene which codes for dihydroxy-acid dehydratase, or
the zwal gene which codes for the Zwal protein; and/or

(B) reduces or eliminates the expression of one or more of the following gene(s):

the pck gene which codes for phosphoenol pyruvate carboxykinase,

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the *pgi* gene which codes for glucose 6-phosphate isomerase,
the *poxB* gene which codes for pyruvate oxidase or
the *zwa2* gene which codes for the Zwa2 protein.

Claim 69 (Currently Amended): An isolated polynucleotide that encodes a polypeptide which is at least 90% identical to SEQ ID NO: 2, which polypeptide has the ~~biological~~ enzymatic activity of adenosyl homocysteinase.

Claim 70 (Previously Presented): The isolated polynucleotide of Claim 69 that encodes a polypeptide which is at least 95% identical to SEQ ID NO: 2.

Claim 71 (Previously Presented): The isolated polynucleotide of Claim 69 that encodes a polypeptide comprising SEQ ID NO: 2.

Claim 72 (Previously Presented): A vector comprising the isolated polynucleotide of Claim 69.

Claim 73 (Previously Presented): A host cell comprising the isolated polynucleotide of Claim 69.

Claim 74 (Previously Presented): A process for producing an amino acid comprising:
culturing the host cell of Claim 73 for a time and under conditions suitable for the production of said amino acid, and
recovering said amino acid.

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Claim 75 (Currently Amended): An isolated polynucleotide which hybridizes to the complement of SEQ ID NO: 1 under stringent conditions and which encodes a polypeptide having the enzymatic activity of adenosyl homocysteinase, and

wherein stringent conditions comprise washing at a temperature ~~ranging from 50°C to~~
of 68°C in 2x SSC.

Claim 76 (Previously Presented): A vector comprising the isolated polynucleotide of Claim 75.

Claim 77 (Previously Presented): A host cell comprising the isolated polynucleotide of Claim 75.

Claim 78 (Previously Presented): A process for producing an amino acid comprising:
culturing the host cell of Claim 77 for a time and under conditions suitable for the
production of said amino acid, and
recovering said amino acid.

Claim 79 (Currently Amended): An isolated polynucleotide ~~comprising~~ consisting of
at least 30 consecutive nucleotides of SEQ ID NO:1, or at least 30 consecutive nucleotides of
the full complement of SEQ ID NO: 1.

Claim 80 (Currently Amended): ~~The~~ An isolated polynucleotide ~~of Claim 79~~ which
~~comprises~~ consists of at least 40 consecutive nucleotides of SEQ ID NO: 1, or at least 40
consecutive nucleotides of the full complement of SEQ ID NO: 1.

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Claim 81 (Currently Amended): ~~The~~ An isolated polynucleotide of ~~Claim 79~~ which ~~comprises~~ consists of at least 50 consecutive nucleotides of SEQ ID NO: 1, or at least 50 consecutive nucleotides of the full complement of SEQ ID NO: 1.

Claim 82 (Previously Presented): *Escherichia coli* strain DH5 α mcx/pEC-XK99sahHalex deposited as DSM 14316.